

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/036,113DATE: 03/18/98
TIME: 11:34:16

INPUT SET: S24228.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

ENTERED

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Cupp, Mary S.
Cupp, Eddie W.

(ii) TITLE OF INVENTION: ANTITHROMBIN PROTEIN AND DNA SEQUENCES

(iii) NUMBER OF SEQUENCES: 2

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: W. Murray Spruill (Alston & Bird, LLP)
(B) STREET: 3605 Glenwood Ave. Suite 310
(C) CITY: Raleigh
(D) STATE: NC
(E) COUNTRY: USA
(F) ZIP: 27622

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Spruill, W. Murray
(B) REGISTRATION NUMBER: 32,943
(C) REFERENCE/DOCKET NUMBER: 5721-5

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 919 420 2202
(B) TELEFAX: 919 881 3175

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 532 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single

RAW SEQUENCE LISTING
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47 (D) TOPOLOGY: linear

48

49 (ii) MOLECULE TYPE: cDNA

50

51 (vi) ORIGINAL SOURCE:

52 (A) ORGANISM: Simulium vittatum

53

54 (ix) FEATURE:

55 (A) NAME/KEY: CDS

56 (B) LOCATION: 1..294

57

58

59 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

60

61 GAG GTG GCG AAT TTG CAG GAC CAT CGA GCT GTT GAA TTT GTG TGC GAG 48

62 Glu Val Ala Asn Leu Gln Asp His Arg Ala Val Glu Phe Val Cys Glu

63 1 5 10 15

64

65 AAG GAT ACT GAA AAC CAG CAT GGT TCC GAT TGC CTG CTT TCT TGT GAC 96

66 Lys Asp Thr Glu Asn Gln His Gly Ser Asp Cys Leu Leu Ser Cys Asp

67 20 25 30

68

69 GTG ATG TTC TGG GAT ACC AAA AAC GAG AAC AAC AAG GAA TAT GAA GAC 144

70 Val Met Phe Trp Asp Thr Lys Asn Glu Asn Asn Lys Glu Tyr Glu Asp

71 35 40 45

72

73 AGA TAC AAT TTG TGC AAA CAT TCA GCC GCT TCC GAA GAG AAC ATT TGT 192

74 Arg Tyr Asn Leu Cys Lys His Ser Ala Ala Ser Glu Glu Asn Ile Cys

75 50 55 60

76

77 GAT CGC AAT GAA GAA TTG AGA GCC TGT TTC TTG CAT GAT TCG TCA TAC 240

78 Asp Arg Asn Glu Glu Leu Arg Ala Cys Phe Leu His Asp Ser Ser Tyr

79 65 70 75 80

80

81 GAA GAG ACT TCG GAC GAA TAT GAA ATA ACC TAC AGC ATG GAT TCC CTG 288

82 Glu Glu Thr Ser Asp Glu Tyr Glu Ile Thr Tyr Ser Met Asp Ser Leu

83 85 90 95

84

85 TGA TGA TCAAACATTG GTAATAGTTC AATTGATCGA AATATGCAGA AACCGTCCAC 344

86 * *

87

88

89 GGTAGTGTA TATAACCCA TGTTGTTTCGC ATTGTACTCT AATTCTACTC CGTTCATATA 404

90

91 TGGCTGATGA GTGCCATCCA GCCAATGTGA AACAGGAGTA TAAAAAGCAC AATGTGGGTG 464

92

93 ACAGTCCCAT TCACACAATA TGCAAATAAA ATAATGGAAA TGACCCCAAA AAAAAAAAAA 524

94

95 AAAAAAAAAA 532

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97

98 (2) INFORMATION FOR SEQ ID NO:2:

99

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100 (i) SEQUENCE CHARACTERISTICS:
101 (A) LENGTH: 96 amino acids
102 (B) TYPE: amino acid
103 (D) TOPOLOGY: linear
104
105 (ii) MOLECULE TYPE: protein
106
107 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
108
109 Glu Val Ala Asn Leu Gln Asp His Arg Ala Val Glu Phe Val Cys Glu
110 1 5 10 15
111
112 Lys Asp Thr Glu Asn Gln His Gly Ser Asp Cys Leu Leu Ser Cys Asp
113 20 25 30
114
115 Val Met Phe Trp Asp Thr Lys Asn Glu Asn Asn Lys Glu Tyr Glu Asp
116 35 40 45
117
118 Arg Tyr Asn Leu Cys Lys His Ser Ala Ala Ser Glu Glu Asn Ile Cys
119 50 55 60
120
121 Asp Arg Asn Glu Glu Leu Arg Ala Cys Phe Leu His Asp Ser Ser Tyr
122 65 70 75 80
123
124 Glu Glu Thr Ser Asp Glu Tyr Glu Ile Thr Tyr Ser Met Asp Ser Leu
125 85 90 95
126
127
128
129

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SEQUENCE VERIFICATION REPORT
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